

FIG. 1

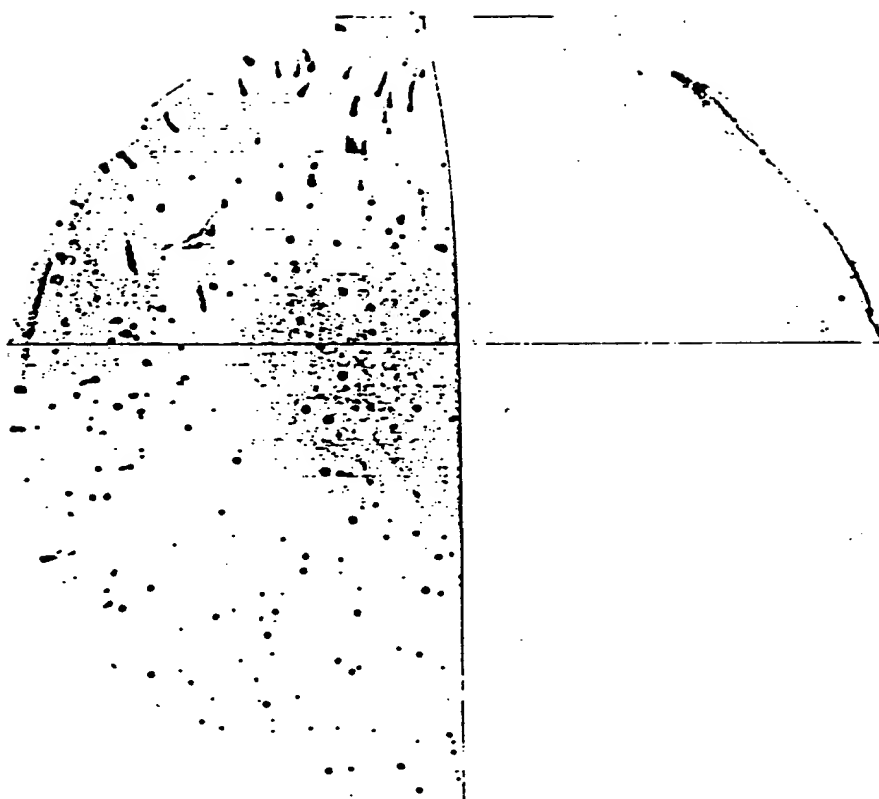
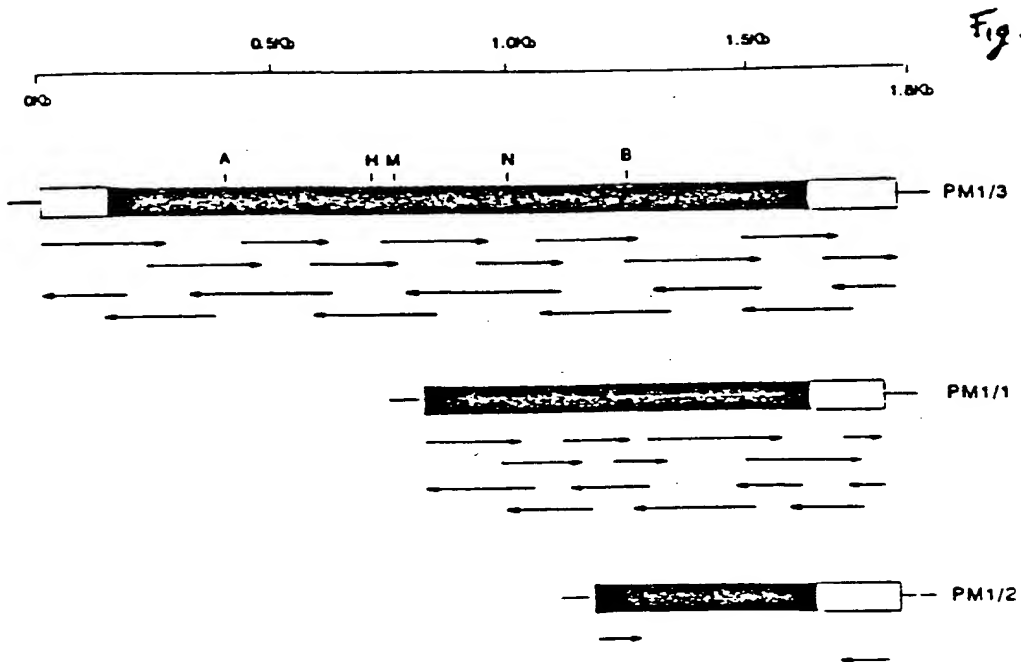


FIG. 2

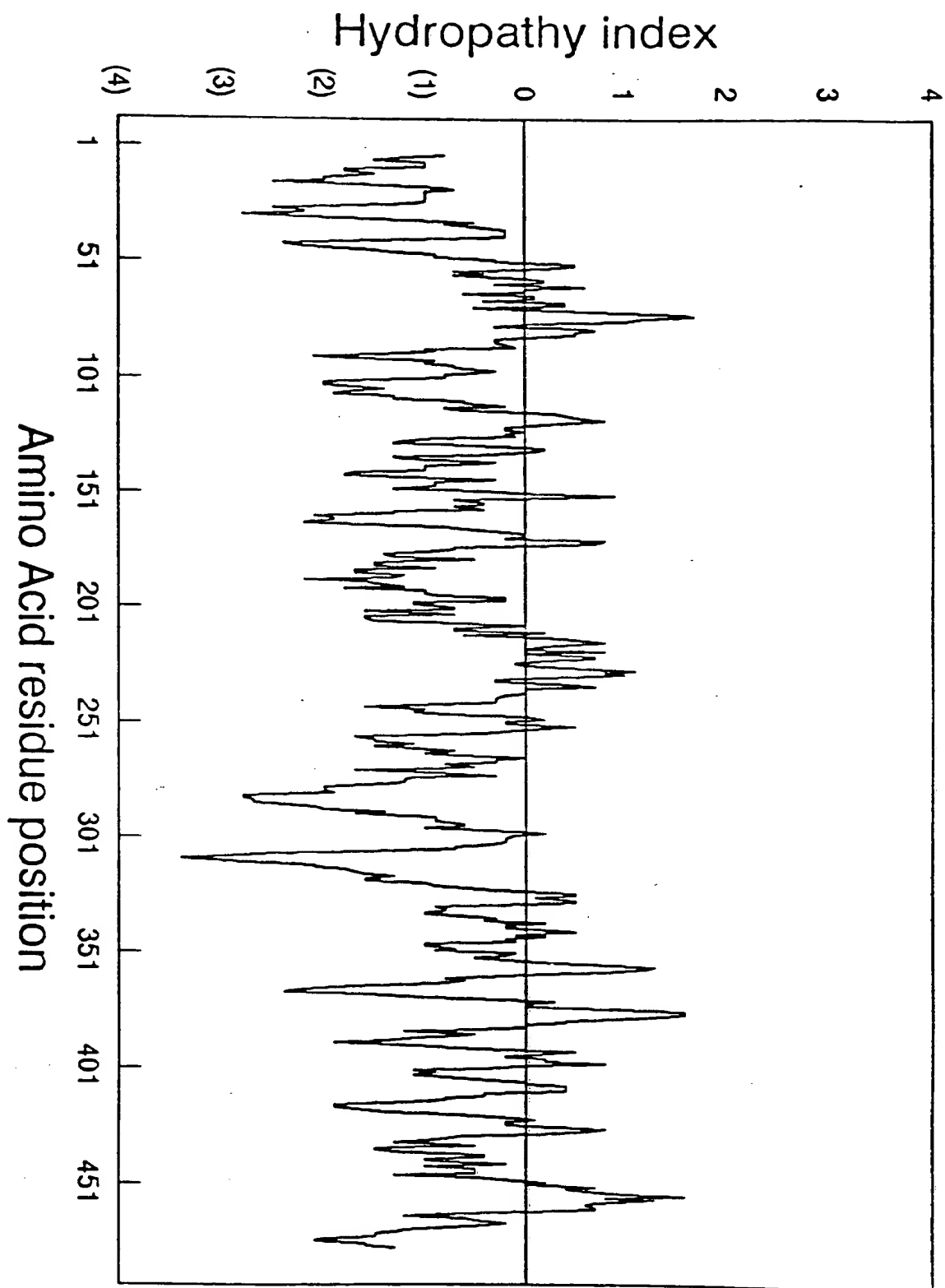
CGGGCGGGGGATACCCCAGGAGATGGGGGTCGAGGAGAGACCCCGGGGAGTAGAGAGAGAGAACTCACTC	71
CCCGAGTCCCCGACCCTCCCCAAGCAAGGTTATAATATAAATTATCCTCTCATGCTTTTTTCTGCCCCCTT	142
CTCCCCAAATCATCAACAATAGAAGAAGAAGAAAACATG TCA GGA CAC AAA TGC AGT TAT CCC	205
Met Ser Gly His Lys Cys Ser Tyr Pro	9
TGG GAC TTA CAG GAT CGA TAT GCT CAA GAT AAG TCA GTT GTA AAT AAG ATG CAA	259
Trp Asp Leu Gln Asp Arg Tyr Ala Gln Asp Lys Ser Val Val Asn Lys Met Gln	27
AMD	
CAG AGA TAT TGG GAG ACG AAG CAG GCC TTT ATT AAA GCC ACA GGG AAG AAG GAA	313
Gln Arg Tyr Trp Glu Thr Lys Gln Ala Phe Ile Lys Ala Thr Gly Lys Lys Glu	45
GAT GAA CAT GTT GTT GCC TCT GAC GCG GAC CTG GAT GCC AAG CTA GAG CTG TTT	367
Asp Glu His Val Val Ala Ser Asp Ala Asp Leu Asp Ala Lys Leu Glu Leu Phe	63
CAT TCA ATT CAG AGA ACC TGT CTG GAC TTA TCG AAA GCA ATT GTA CTC TAT CAA	421
His Ser Ile Gln Arg Thr Cys Leu Asp Leu Ser Lys Ala Ile Val Leu Tyr Gln	81
CK2	
AAG AGG ATA TGT TTC TTG TCT CAA GAA GAA AAC GAA CTG GGA AAA TTT CTT CGA	475
Lys Arg Ile Cys Phe Leu Ser Gln Glu Glu Asn Glu Leu Gly Lys Phe Leu Arg	99
TCC CAA GGT TTC CAA GAT AAA ACC AGA GCA GGA AAG ATG ATG CAA GCG ACA GGA	529
Ser Gln Gly Phe Gln Asp Lys Thr Arg Ala Gly Lys Met Met Gln Ala Thr Gly	117
AAG GCC CTC TGC TTT TCT TCC CAG CAA AGG TTG GCC TTA CGA AAT CCT TTG TGT	583
Lys Ala Leu Cys Phe Ser Ser Gln Gln Arg Leu Ala Leu Arg Asn Pro Leu Cys	135
CGA TTT CAC CAA GAA GTG GAG ACT TTT CGG CAT CGG GCC ATC TCA GAT ACT TGG	637
Arg Phe His Gln Glu Val Glu Thr Phe Arg His Arg Ala Ile Ser Asp Thr Trp	153
CTG ACG GTG AAC CGC ATG GAA CAG TGC AGG ACG GAA TAT AGA GGA GCA CTA TTA	691
Leu Thr Val Asn Arg Met Glu Gln Cys Arg Thr Glu Tyr Arg Gly Ala Leu leu	171
TGG ATG AAG GAC GTG TCT CAG GAG CTT GAT CCA GAC CTC TAC AAG CAA ATG GAG	745
Trp Met Lys Asp Val Ser Gln Glu Leu Asp Pro Asp Leu Tyr Lys Gln Met Glu	189
AAG TTC AGG AAG GTG CAA ACA CAA GTG CGC CTT GCA AAA AAA AAC TTT GAC AAA	799
Lys Phe Arg Lys Val Gln Thr Gln Val Arg Leu Ala Lys Lys Asn Phe Asp Lys	207
TTG AAG ATG GAT GTG TGT CAA AAA GTG GAT CTT CTT GGA GCG AGC AGA TGC AAT	853
Leu Lys Met Asp Val Cys Gln Lys Val Asp Leu Leu Gly Ala Ser Arg Cys Asn	225
CTC TTG TCT CAC ATG CTA GCA ACA TAC CAG ACC ACT CTG CTT CAT TTT TGG GAG	907
Leu Leu Ser His Met Leu Ala Thr Tyr Gln Thr Thr Leu Leu His Phe Trp Glu	243
PKC	
AAA ACT TCT CAC ACT ATG GCA GCC ATC CAT GAG AGT TTC AAA GGT TAT CAA CCA	961
Lys Thr Ser His Thr Met Ala Ala Ile His Glu Ser Phe Lys Gly Tyr Gln Pro	261
CK2	
TAT GAA TTT ACT ACT TTA AAG AGC TTA CAA GAC CCT ATG AAA AAA TTA GTT GAG	1015
Tyr Glu Phe Thr Thr Leu Lys Ser Leu Gln Asp Pro Met Lys Lys Leu Val Glu	279
AAA GAA GAG AAG AAG AAA ATC AAC CAG CAG GAA AGT ACA GAT GCA GCC GTG CAG	1069
Lys Glu Glu Lys Lys Lys Ile Asn Gln Gln Glu Ser Thr Asp Ala Ala Val Gln	297

CCCCTGGGGGCTAGCAGAAGTATAAAGTGATCAGTATGCTGTTTTAATAATTATGTGCCATTTTAATAAAA 1745
FGAAAGGGTCAACGGCCCTGTTAAAAAAAAAAAAAAAAAAAA 1785



N	F D K L K	M D V	C	PM-1	205
V	F D K L K	H L V	D	BSA	373

S	E E	G A C L	G P	V	PM-1	351
E	D K	G A C L	P K	BSA	172	



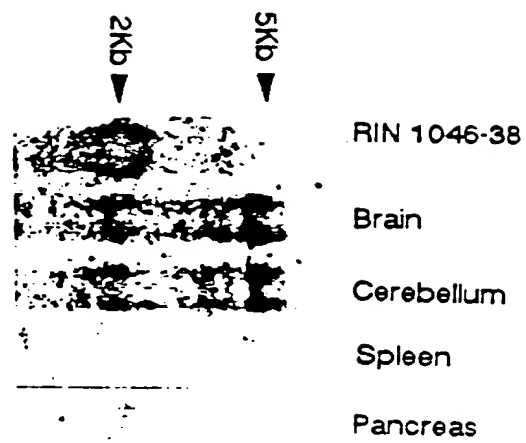


FIG. 7

